IN THE CLAIMS

1-59. (canceled)

60. (previously presented) A hypermutable transgenic mouse wherein at least 50% of the cells of said mouse comprise a dominant negative allele of a *PMS2* mismatch repair gene, wherein said dominant negative allele comprises a truncation mutation.

61. (currently amended) A hypermutable, transgenic mouse produced by a process comprising the steps of:

introducing a polynucleotide comprising a sequence encoding a dominant negative allele of a *PMS2* mismatch repair gene into ~~said~~ a fertilized mouse egg, wherein the dominant negative allele comprises a truncation mutation, whereby said fertilized mouse egg becomes hypermutable; and

allowing said mouse egg to develop into a hypermutable, transgenic mouse.

62. (currently amended) A method of making a hypermutable, fertilized mouse egg comprising introducing into said ~~murine~~ fertilized mouse egg a polynucleotide comprising a sequence encoding a dominant negative allele of a *PMS2* mismatch repair gene, wherein the dominant negative allele comprises a truncation mutation, whereby said ~~murine~~ fertilized mouse egg becomes hypermutable.

63-69. (canceled)

70. (currently amended) The ~~method~~ mouse of claim ~~69~~ 61 wherein the fertilized egg is ~~subsequently~~ implanted into a pseudopregnant female mouse ~~whereby the fertilized egg develops into a mature transgenic mouse~~.

71. (currently amended) A method for generating a mutation in a gene of interest comprising the steps of:

introducing a polynucleotide comprising a dominant negative allele of a *PMS2* mismatch repair gene into a fertilized mouse egg, wherein the dominant negative allele comprises a truncation mutation, whereby the fertilized mouse egg becomes hypermutable;

~~growing a~~ allowing said fertilized mouse egg to develop into a hypermutable, transgenic mouse ~~comprising the gene of interest and a polynucleotide encoding a dominant negative allele of a *PMS2* mismatch repair gene, wherein the dominant negative allele comprises a truncation mutation~~; and

testing the mouse to determine whether the gene of interest harbors a mutation.

72. (previously presented) The method of claim 71 wherein the step of testing comprises analyzing a nucleotide sequence of the gene of interest.

73. (previously presented) The method of claim 71 wherein the step of testing comprises analyzing mRNA transcribed from the gene of interest.

74. (previously presented) The method of claim 71 wherein the step of testing comprises analyzing a protein encoded by the gene of interest.

75. (previously presented) The method of claim 71 wherein the step of testing comprises analyzing the phenotype of the gene of interest.

76-80. (canceled)

81. (new) The method of claim 62 wherein the mismatch repair gene is human *PMS2*.

82. (new) The method of claim 81 wherein said mismatch repair gene comprises a truncation mutation at codon 134 as shown in SEQ ID NO:1.

83. (new) The method of claim 82 wherein the truncation mutation is a thymidine at nucleotide 424 of wild-type *PMS2* as shown in SEQ ID NO:1.

84. (new) The hypermutable, transgenic mouse of claim 60 comprising a protein which consists of the first 133 amino acids of human PMS2.

85. (new) The hypermutable, transgenic mouse of claim 61 wherein the mismatch repair gene is human *PMS2*.

86. (new) The hypermutable, transgenic mouse of claim 61 wherein the dominant negative allele comprises a truncation mutation at codon 134 as shown in SEQ ID NO:1.

87. (new) The hypermutable, transgenic mouse of claim 86 wherein the truncation mutation is a thymidine at nucleotide 424 of wild-type *PMS2* as shown in SEQ ID NO:1.

IN THE SPECIFICATION

On page 1, delete the paragraph after the title and substitute the following paragraph:

This application is a division of U.S. Serial No. 09/059,461, filed April 14, 1998, now U.S. Patent 6,146,894 ~~allowed~~.